

APR 23 2003

TECH CE



1600

## RAW SEQUENCE LISTING

DATE: 04/18/2003

PATENT APPLICATION: US/08/813,323C

TIME: 14:26:36

Input Set : N:\Crf4\04152003\H813323.raw

Output Set: N:\CRF4\04182003\H813323C.raw

1 <110> APPLICANT: Baltimore, David  
2 Cheng, Genhong  
3 Ye, Zheng-Sheng  
4 Lederman, Seth  
5 Cleary, Aileen  
6 <120> TITLE OF INVENTION: Truncated CraF-1 Inhibits CD40 Signalling  
7 <130> FILE REFERENCE: 0575/50659  
8 <140> CURRENT APPLICATION NUMBER: US/08/813,323C  
9 <141> CURRENT FILING DATE: 1997-03-10  
10 <160> NUMBER OF SEQ ID NOS: 11  
11 <170> SOFTWARE: PatentIn version 3.1  
13 <210> SEQ ID NO: 1  
14 <211> LENGTH: 567  
15 <212> TYPE: PRT  
16 <213> ORGANISM: Mouse Sp.  
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20 Pro Pro Leu Lys Leu Gln Pro Asp Arg Gly Ala Gly Ser Val Leu Val  
21 20 25 30  
22 Pro Glu Gln Gly Gly Tyr Lys Glu Lys Phe Val Lys Thr Val Glu Asp  
23 35 40 45  
24 Lys Tyr Lys Cys Glu Lys Cys Arg Leu Val Leu Cys Asn Pro Lys Gln  
25 50 55 60  
26 Thr Glu Cys Gly His Arg Phe Cys Glu Ser Cys Met Ala Ala Leu Leu  
27 65 70 75 80  
28 Ser Ser Ser Ser Pro Lys Cys Thr Ala Cys Gln Glu Ser Ile Ile Lys  
29 85 90 95  
30 Asp Lys Val Phe Lys Asp Asn Cys Cys Lys Arg Glu Ile Leu Ala Leu  
31 100 105 110  
32 Gln Val Tyr Cys Arg Asn Glu Gly Arg Gly Cys Ala Glu Gln Leu Thr  
33 115 120 125  
34 Leu Gly His Leu Leu Val His Leu Lys Asn Glu Cys Gln Phe Glu Glu  
35 130 135 140  
36 Leu Pro Cys Leu Arg Ala Asp Cys Lys Glu Lys Val Leu Arg Lys Asp  
37 145 150 155 160  
38 Leu Arg Asp His Val Glu Lys Ala Cys Lys Tyr Arg Glu Ala Thr Cys  
39 165 170 175  
40 Ser His Cys Lys Ser Gln Val Pro Met Ile Lys Leu Gln Lys His Glu  
41 180 185 190  
42 Asp Thr Asp Cys Pro Cys Val Val Val Ser Cys Pro His Lys Cys Ser  
43 195 200 205  
44 Val Gln Thr Leu Leu Arg Ser Glu Leu Ser Ala His Leu Ser Glu Cys

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45          210          215          220
46 Val Asn Ala Pro Ser Thr Cys Ser Phe Lys Arg Tyr Gly Cys Val Phe
47 225          230          235          240
48 Gln Gly Thr Asn Gln Ile Lys Ala His Glu Ala Ser Ser Ala Val
49          245          250          255
50 Gln His Val Asn Leu Leu Lys Glu Trp Ser Asn Ser Leu Glu Lys Lys
51          260          265          270
52 Val Ser Leu Leu Gln Asn Glu Ser Val Glu Lys Asn Lys Ser Ile Gln
53          275          280          285
54 Ser Leu His Asn Gln Ile Cys Ser Phe Glu Ile Glu Ile Glu Arg Gln
55          290          295          300
56 Lys Glu Met Leu Arg Asn Asn Glu Ser Lys Ile Leu His Leu Gln Arg
57 305          310          315          320
58 Val Ile Asp Ser Gln Ala Glu Lys Leu Lys Glu Leu Asp Lys Glu Ile
59          325          330          335
60 Arg Pro Phe Arg Gln Asn Trp Glu Glu Ala Asp Ser Met Lys Ser Ser
61          340          345          350
62 Val Glu Ser Leu Gln Asn Arg Val Thr Glu Leu Glu Ser Val Asp Lys
63          355          360          365
64 Ser Ala Gly Gln Ala Ala Arg Asn Thr Gly Leu Leu Glu Ser Gln Leu
65          370          375          380
66 Ser Arg His Asp Gln Thr Leu Ser Val His Asp Ile Arg Leu Ala Asp
67 385          390          395          400
68 Met Asp Leu Arg Phe Gln Val Leu Glu Thr Ala Ser Tyr Asn Gly Val
69          405          410          415
70 Leu Ile Trp Lys Ile Arg Asp Tyr Lys Arg Arg Lys Gln Glu Ala Val
71          420          425          430
72 Met Gly Lys Thr Leu Ser Leu Tyr Ser Gln Pro Phe Tyr Thr Gly Tyr
73          435          440          445
74 Phe Gly Tyr Lys Met Cys Ala Arg Val Tyr Leu Asn Gly Asp Gly Met
75          450          455          460
76 Gly Lys Gly Thr His Leu Ser Leu Phe Phe Val Ile Met Arg Gly Glu
77 465          470          475          480
78 Tyr Asp Ala Leu Leu Pro Trp Pro Phe Lys Gln Lys Val Thr Leu Met
79          485          490          495
80 Leu Met Asp Gln Gly Ser Ser Arg Arg His Leu Gly Asp Ala Phe Lys
81          500          505          510
82 Pro Asp Pro Asn Ser Ser Ser Phe Lys Lys Pro Thr Gly Glu Met Asn
83          515          520          525
84 Ile Ala Ser Gly Cys Pro Val Phe Val Ala Gln Thr Val Leu Glu Asn
85          530          535          540
86 Gly Thr Tyr Ile Lys Asp Asp Thr Ile Phe Ile Lys Val Ile Val Asp
87 545          550          555          560
88 Thr Ser Asp Leu Pro Asp Pro
89          565

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91 &lt;210&gt; SEQ ID NO: 2

92 &lt;211&gt; LENGTH: 568

93 &lt;212&gt; TYPE: PRT

94 &lt;213&gt; ORGANISM: Homo Sapiens

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95 &lt;400&gt; SEQUENCE: 2

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96 Met Glu Ser Ser Lys Lys Met Asp Ser Pro Gly Ala Leu Gln Thr Asn
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98 Pro Pro Leu Lys Leu His Thr Asp Arg Ser Ala Gly Thr Pro Val Phe
99 20 25 30
100 Val Pro Glu Gln Gly Gly Tyr Lys Glu Lys Phe Val Lys Thr Val Glu
101 35 40 45
102 Asp Lys Tyr Lys Cys Glu Lys Cys His Leu Val Leu Cys Ser Pro Lys
103 50 55 60
104 Gln Thr Glu Cys Gly His Arg Phe Cys Glu Ser Cys Met Ala Ala Leu
105 65 70 75 80
106 Leu Ser Ser Ser Ser Pro Lys Cys Thr Ala Cys Gln Glu Ser Ile Val
107 85 90 95
108 Lys Asp Lys Val Phe Lys Asp Asn Cys Cys Lys Arg Glu Ile Leu Ala
109 100 105 110
110 Leu Gln Ile Tyr Cys Arg Asn Glu Ser Arg Gly Cys Ala Glu Gln Leu
111 115 120 125
112 Thr Leu Gly His Leu Leu Val His Leu Lys Asn Asp Cys His Phe Glu
113 130 135 140
114 Glu Leu Pro Cys Val Arg Pro Asp Cys Lys Glu Lys Val Leu Arg Lys
115 145 150 155 160
116 Asp Leu Arg Asp His Val Glu Lys Ala Cys Lys Tyr Arg Glu Ala Thr
117 165 170 175
118 Cys Ser His Cys Lys Ser Gln Val Pro Met Ile Ala Leu Gln Lys His
119 180 185 190
120 Glu Asp Thr Asp Cys Pro Cys Val Val Ser Cys Pro His Lys Cys
121 195 200 205
122 Ser Val Gln Thr Leu Leu Arg Ser Glu Leu Ser Ala His Leu Ser Glu
123 210 215 220
124 Cys Val Asn Ala Pro Ser Thr Cys Ser Phe Lys Arg Tyr Gly Cys Val
125 225 230 235 240
126 Phe Gln Gly Thr Asn Gln Gln Ile Lys Ala His Glu Ala Ser Ser Ala
127 245 250 255
128 Val Gln His Val Asn Leu Leu Lys Glu Trp Ser Asn Ser Leu Glu Lys
129 260 265 270
130 Lys Val Ser Leu Leu Gln Asn Glu Ser Val Glu Lys Asn Lys Ser Ile
131 275 280 285
132 Gln Ser Leu His Asn Gln Ile Cys Ser Phe Glu Ile Glu Ile Glu Arg
133 290 295 300
134 Gln Lys Glu Met Leu Arg Asn Asn Glu Ser Lys Ile Leu His Leu Gln
135 305 310 315 320
136 Arg Val Ile Asp Ser Gln Ala Glu Lys Leu Lys Glu Leu Asp Lys Glu
137 325 330 335
138 Ile Arg Pro Phe Arg Gln Asn Trp Glu Glu Ala Asp Ser Met Lys Ser
139 340 345 350
140 Ser Val Glu Ser Leu Gln Asn Arg Val Thr Glu Leu Glu Ser Val Asp
141 355 360 365
142 Lys Ser Ala Gly Gln Val Ala Arg Asn Thr Gly Leu Leu Glu Ser Gln
143 370 375 380

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144   Leu Ser Arg His Asp Gln Met Leu Ser Val His Asp Ile Arg Leu Ala
145   385                               390                               395                               400
146   Asp Met Asp Leu Arg Phe Gln Val Leu Glu Thr Ala Ser Tyr Asn Gly
147                               405                               410                               415
148   Val Leu Ile Trp Lys Ile Arg Asp Tyr Lys Arg Arg Lys Gln Glu Ala
149                               420                               425                               430
150   Val Met Gly Lys Thr Leu Ser Leu Tyr Ser Gln Pro Phe Tyr Thr Gly
151                               435                               440                               445
152   Tyr Phe Gly Tyr Lys Met Cys Ala Arg Val Tyr Leu Asn Gly Asp Gly
153   450                               455                               460
154   Met Gly Lys Gly Thr His Leu Ser Leu Phe Phe Val Ile Met Arg Gly
155   465                               470                               475                               480
156   Glu Tyr Asp Ala Leu Leu Pro Trp Pro Phe Lys Gln Lys Val Thr Leu
157                               485                               490                               495
158   Met Leu Met Asp Gln Gly Ser Ser Arg Arg His Leu Gly Asp Ala Phe
159                               500                               505                               510
160   Lys Pro Asp Pro Asn Ser Ser Ser Phe Lys Lys Pro Thr Gly Glu Met
161                               515                               520                               525
162   Asn Ile Ala Ser Gly Cys Pro Val Phe Val Ala Gln Thr Val Leu Glu
163   530                               535                               540
164   Asn Gly Thr Tyr Ile Lys Asp Asp Thr Ile Phe Ile Lys Val Ile Val
165   545                               550                               555                               560
166   Asp Thr Ser Asp Leu Pro Asp Pro
167                               565

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169 &lt;210&gt; SEQ ID NO: 3

170 &lt;211&gt; LENGTH: 2359

171 &lt;212&gt; TYPE: DNA

172 &lt;213&gt; ORGANISM: Mouse Sp.

173 &lt;400&gt; SEQUENCE: 3

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175   tccccattac ttgaaggata aggctggcac ggctccgacg tctgtgtgga agcttctccc      120
176   tcccttctga gcttctctag actccttaca gcgcacggca cagaatttca gtttcctaag      180
177   atggagtcaa gcaaaaagat ggatgctgct ggcacactgc agcctaaccc acccctaaag      240
178   ctgcagcctg atcgcggcgc aggggtccgtg ctggtgccgg agcaaggagg ctacaaggag      300
179   aagtttgtga agacggtgga agacaagtac aagtgcgaga agtgccgcct ggtgctgtgc      360
180   aaccogaagc agacggagtg tggccaccgg ttctgcgaga gctgcatggc cgccctgctg      420
181   agctcctcca gtccaaaatg cacagcgtgc caagaaagca tcatcaaaga caagggtgtt      480
182   aaggataatt gctgcaagag agagattctg gcccttcagg tctactgtcg gaatgaaggc      540
183   agaggttgtg cggagcagct gactctggga catctgctgg tgcacctaaa aaatgaatgt      600
184   cagtttgagg aacttccctg tctgcgtgcc gactgcaaag aaaaagtact gagaaaagac      660
185   ttgcgggata acgtggaaaa ggctgtaaa taccgcgagg ccacgtgcag tcaactgcaag      720
186   agccaagtgc ccatgatcaa actgcagaaa catgaagaca cagattgtcc ctgtgtggtg      780
187   gtatcctgcc ctcacaagtg cagcgttcag actcttctaa ggagtgaagt gagtgcacac      840
188   ttgtccgagt gtgtcaatgc cccagcacc tgtagtttta agcgtatgg ctgctgtttt      900
189   cagggtaaca accagcagat caaggccat gaggccagct ccgcggtaca gcacgtgaac      960
190   ctgctgaagg agtgagcaaa ctccctggag aagaaggttt ccctgctgca gaatgaaagt     1020
191   gttgagaaaa acaagagcat ccaaagcctg cacaaccaga tctgcagctt tgagatcgag     1080
192   attgagaggc agaaggagat gctccgaaac aacgagtcca agatccttca cctgcagcgg     1140
193   gtaatcgaca gccaaagcaga gaaactgaaa gaactggaca aggagatccg tcccttccgg     1200

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196	gagtcccagc	tgagccggca	tgaccagacg	ttgagtgttc	atgacatccg	cttggccgac	1380
197	atggacctgc	ggttccaggt	cctcgagacc	gccagctaca	acggggtgct	gatctggaag	1440
198	atccgtgact	acaagcgccg	gaagcaggag	gccgtcatgg	ggaagaccct	gtctctctac	1500
199	agccagcctt	tctacacagg	ttattttggc	tataagatgt	gtgccagggt	ctacctgaat	1560
200	ggggacggaa	tggggaaagg	gacacacttg	tcgctgtttt	ttgtcattat	gcgtggagaa	1620
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202	gggtcctctc	gccgtcatct	gggagatgcg	ttcaagcctg	accccaacag	cagcagcttc	1740
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204	gttctagaga	acgggacgta	tattaaagat	gatacaatct	ttattaaggt	catagtggat	1860
205	acctcggatc	tgctgacccc	ctgacaagaa	agcaggcgcg	tggattcagc	agaaggtaac	1920
206	tcctctgggg	gggtgagcta	gtgtcttcac	ggaggtcctc	gccctcagaa	aggaccttgt	1980
207	ggcgagagg	aagcagccgg	aggaggagaa	ggaggtcgag	tggctggcag	gagagccaca	2040
208	tgtgaaaaca	gaccccaacg	gattttctaa	taaactagcc	acacccactc	tgaaggatta	2100
209	tttatccatc	aacaagataa	atactgctgt	cagagaaggt	tttcattttc	attttaaaag	2160
210	atctagtatt	aaggtgggaa	catatatgct	aaaaagaaac	atgatttttc	ttccttaact	2220
211	taaacaccaa	aaagagaaca	catgtggggg	tagctggagt	gtgtacagta	cctcgagggc	2280
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222	ccggggagca	gaacgctgcg	gaccgcggcg	gaggacgcgc	ccggcgcccc	tgagccggcc	180
223	gagcggcgac	ggaccgcgag	aactcctctt	tcctaaaatg	gagtcgagta	aaaagatgga	240
224	ctctcctggc	gcgctgcaga	ctaaccgcgc	gctaaagctg	cacactgacc	gtagtgtgg	300
225	gacgccagtt	tttgtccctg	aacaaggagg	ttacaaggaa	aagtttgtga	agaccgtgga	360
226	ggacaagtac	aagtgtgaga	agtgccacct	ggtgctgtgc	agcccgaagc	agaccgagtg	420
227	tgggcaccgc	ttctgcgaga	gctgcatggc	ggccctgctg	agctcttcaa	gtccaaaatg	480
228	tacagcgtgt	caagagagca	tcgttaaaga	taagggtgtt	aaggataatt	gctgcaagag	540
229	agaaattctg	gctcttcaga	tctattgtcg	gaatgaaagc	agaggttgtg	cagagcagtt	600
230	aacgctggga	catctgctgg	tgcatttaaa	aaatgattgc	cattttgaag	aacttccatg	660
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232	ggcgtgtaaa	taccgggaag	ccacatgcag	ccactgcaag	agtcagggtc	cgatgatcgc	780
233	gctgcagaaa	cacgaagaca	ccgactgtcc	ctgcgtgggt	gtgtcctgcc	ctcacaagtg	840
234	cagcgtccag	actctcctga	ggagcgagtt	gagtgcacac	ttgtcagagt	gtgtcaatgc	900
235	ccccagcacc	tgtagtttta	agcgtatggt	ctgcgttttt	caggggacaa	accagcagat	960
236	caaggcccac	gaggccagct	ccgcctgca	gcacgtcaac	ctgctgaagg	agtggagcaa	1020
237	ctcgctcgaa	aagaaggttt	ccttggttga	gaatgaaagt	gtagaaaaaa	acaagagcat	1080
238	acaaagtttg	cacaatcaga	tatgtagctt	tgaaattgaa	attgagagac	aaaaggaaat	1140
239	gcttcgaaat	aatgaatcca	aaatccttca	tttacagcga	gtgatcgaca	gccaagcaga	1200
240	gaaactgaag	gagcttgaca	aggagatccg	gcccttcogg	cagaactggg	aggaagcaga	1260
241	cagcatgaag	agcagcgtgg	agtccctcca	gaaccgcgtg	accgagctgg	agagcgtgga	1320
242	caagagtgcg	gggcaagtgg	ctcggaacac	aggcctgctg	gagtcccagc	tgagccggca	1380
243	tgaccagatg	ctgagtgtgc	acgacatccg	cctagccgac	atggacctgc	gcttccaggt	1440

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